

1 CCCACGGCTC CGCATAAATC AGCAGCGGC CGGAGAACC CGCAATCTCT GCGCCACAA AATACACCGA CGATGCCGA TCTACTTTAA GGGCTGAAAC
GGGTGCGCAG GCGTATTTAG TCGTGCGCCG GCCTCTTGGG GCGTTAGAGA CCGGGTGT TTATGTGGCT GCTACGGGCT AGATGAAATT CCCGACTTTG
101 CCACGGGCCT GAGAGACTAT AAGAGCGTTC CTTACCGCCA TGGAAACAAC GGGACAGAAC GCCCCGGCCG CTTTCGGGGG CCGGAAAAGG CACGGCCCCAG
GGTGCCCCGA CTCTCTGATA TTCTCGCAAG GGATGGCGGT ACCTTGTTC CCCTGTCTTG CCGGGCCGGC GAAGCCCCG GGCCTTTTCC GTGCCGGGTC
2 M etGluGlnAr gGlyGlnAsn AlaProAlaA laSerGlyAl aArgLysArg HisGlyProGly
201 GACCCAGGGA GCGCGGGGA GCCAGGCCTG GCTCCGGGT CCCAAGACC CTTGTGCTCG TTGTGCGCCG GTTCTCTGCTG TTGGTCTCAG CTGAGTCTGC
CTGGGTCCCT CCGCGCCCT CCGTCCGGAC CCGAGGCCA GGGTTCTGG GAAACAGAGC AACAGCGCG CCAGGACGAC AACACAGATC GACTCAGACG
22 ProArgG1 uAlaArgGly AlaArgProG lyLeuArgVa lProLysThr LeuValLeuV alValAlaAl aValLeuLeu LeuValSerA laGluSerAla
301 TCTGATCACC CAACAAGACC TAGTCCCA TAGTCCCA GCAGAGAGC GCCCCACAAC AAAAGAGGTC CAGCCCCCTCA GAGGGATTGT GTCCACCTGG ACACCATATC
AGACTAGTGG GTTGTCTGG ATCGAGGGGT CGTCTCTCGC CCGGGTGTG TTTTCTCCAG GTCGGGAGT CTCCTTAACA CAGGTGGACC TGTGGTATAG
55 LeuLeuThr GlnGlnAspL euAlaProG1 nGlnArgAla AlaProGlnG lnLysArgSe rSerProSer GluGlyLeuC ysProProG1 yHisHisIle
401 TCAGAAGACG GTAGAGATTG CATCTCTCGC AAATATGGAC AGGACTATAG CACTCACTGG AATGACCTCC TTTTCTGCTT GCGCTGCACC AGGTGTGATT
AGTCTTCTGC CATCTCTAAC GTAGAGGACG TTTATACCTG TCCTGATATC GTGAGTGACC TTACTGGAGG AAAAGACGAA CCGACGTGG TCCACACTAA
88 SerGluAspG lyArgAspCy sIleSerCys LysTyrGlyG lnAspTyrSe rThrHisTrp AsnAspLeuL euPheCysLe uArgCysThr ArgCysAspSer
501 CAGGTGAAGT GGAGCTAAGT CCCTGCACCA CGACCAGAAA CACAGTGTGT CAGTGCAGAG AAGGCACCTT CCGGGAAGAA GATTCTCTCTG AGATGTGCCG
GTCCACTTCA CCTCGATTCA GGGACGTGGT GCTGGTCTTT GTGTACACA GTACAGCTTC TTCCGTGGAA GGCCCTTCTT CTAAGAGGAC TCTACACGGC
122 GlyGluVa lGluLeuSer ProCysThrT hrThrArgAs nThrValCys GlnCysGluG luGlyThrPh eArgGluGlu AspSerProG luMetCysArg
601 GAAGTCCCG ACAGGGTGT CCAGAGGGAT GGTCAAGGTC GGTGATTGTA CACCTCGAG TGACATCGAA TGTGTCCACA AAGAATCAGG CATCATCATA
CTTCACGGCG TGTCCACAG GGTCTCCCTA CAGTTCCTC CCACTAACAT GTGGGACCTC ACTGTAGCTT ACACAGGTGT TTCTTAGTCC GTAGTAGTAT
155 LysCysArg ThrGlyCysP roArgGlyMe tValLysVal GlyAspCysT hrProTrpSe rAspIleGlu CysValHisL ysGluSerG1 yIleIleIle
701 GGAGTCACAG TTGCAGCCGT AGTCTTGATT GTGGCTGTGT TTGTTTGCAA GTCTTTACTG TGAAGAAAG TCCTTCTCTTA CCTGAAAAGG ATCTGCTCAG
CCTCAGTGT CACGTGGCA TCAGAACTAA CACCGACACA AACAAACGTT CAGAAATGAC ACCTTCTTTC AGGAAGGAAT GGACTTTCCG TAGACGAGTC
188 GlyValThrV alAlaAlaVa lValLeuIle ValAlaValP heValCysLy sSerLeuLeu TrpLysLysV alLeuProTy rLeuLysGly IleCysSerGly
801 GTGTGGTGG GGACCTGAG CGTGTGGACA GAAGCTCACA ACGACCTGG GCTGAGGACA ATGTCTCTCAA TGAGATCGTG AGTATCTTGC AGCCACCCCA
CACCACCACC CCTGGGACT GCACACCTGT CTTCGAGTGT TGCTGGACCC CGACTCTGT TACAGGAGTT ACTCTAGCAC TCATAGAACG TCGGGTGGGT
222 GlyGlyG1 yAspProGlu ArgValAspA rgSerSerG1 nArgProGly AlaGluAspA snValLeuAs nGluIleVal SerIleLeuG lnProThrGln

FIG. 1A

901 GGTCCTCTGAG CAGGAAATGG AAGTCCAGGA GCCAGCAGAG CCAACAGGTG TCAACATGTT GTCCCCCGGG GAGTCAGAGC ATCTGCTGGA ACCGGCAGAA
 CCAGGGACTC GTCCCTTTACC TTCAGGTCCT CGGTCTCTC AGTTGTCCAC AGTTGTCCAC CAGGGGGCCC CTCAGTCTCG TAGACGACCT TGGCCGTCTT
 255 ValProGlu GlnGluMetG luValGlnG1 uProAlaGlu ProThrGlyV alAsnMetLe userProGly GluSerGluH isLeuLeuG1 uProAlaGlu
 1001 GCTGAAAGGT CTCAGAGGAG GAGGCTGCTG GTTCCAGCAA ATGAAGGTGA TCCCACTGAG ACTCTGAGAC AGTGTTCGA TGACTTTGCA GACTTGGTGC
 CGACTTTCCA GAGTCTCCTC CTCGACGAC CAAGTCTGTT TACTTCCACT AGGTGACTC TGAGACTCTG TCACGAAGCT ACTGAAACGT CTGAACCACG
 288 AlaGluArgS erGlnArgAr gArgLeuLeu ValProAlaA snGluGlyAs pProThrGlu ThrLeuArgG lnCysPheAs pAspPheAla AspLeuValPro
 1101 CCTTTGACTC CTGGGAGCCG CTCATGAGGA AGTTGGGCCT CATGGACAAT GAGATAAAGG TGGCTAAAGC TGAGGCAGCG GGCCACAGGG ACACCTTGTA
 GGAAACTGAG GACCCTCGGC GAGTACTCCT TCAACCCCGA GTACCTGTTA CTCtATTTCC ACCGATTTCG ACTCCGTCCG CCGGTGTCCC TGTGGAACAT
 322 PheaspSe rTrpGluPro LeuMetArgL ysLeuGlyLe uMetAspAsn GluIleLysV alAlaLysAl aGluAlaAla GlyHisArgA spThrLeuTyr
 1201 CACGATGCTG ATAAAGTGGG TCAACAAAAC CGGGCGAGAT GCCTCTGTCC ACACCCTGCT GGATGCCTTG GAGACGCTGG GAGAGAGACT TGCCAAGCAG
 GTGCTACGAC TATTTCACCC AGTTGTTTTG GCCCGCTCTA CGGAGACAGG TGTGGGACGA CCTACGGAAC CTCTGCGACC CTCTCTCTGA ACGGTTCGTC
 355 ThrMetLeu IleLysTrpV alAsnLysTh rGlyArgAsp AlaSerValH isThrLeuLe uAspAlaLeu GluThrLeuG lyGluArgLe uAlaLysGln
 1301 AAGATTGAGG ACCACTTGTT GAGCTCTGGA AAGTTCATGT ATCTAGAAAG TAATGCAGAC TCTGCCWTGT CCTAAGTGTG ATTCTCTTCA GGAAGTGAGA
 TTCTAACTCC TGGTGAACAA CTCGAGACCT TTCAAGTACA TAGATCTTCC ATTACGTCTG AGACGGAACA GGATTTCACAC TAAGAGAAAGT CCTTCACCTCT
 388 LysIleGluA spHisLeuLe uSerSerGly LysPheMetT yrLeuGluG1 yAsnAlaAsp SerAlaXaaS erOC*
 1401 CCTTCCCTGG TTTACCTTTT TTCTGGAAAA AGCCCAACTG GACTCCAGTC AGTAGGAAAG TGCCACAATT GTCACATGAC CGGTACTGGA AGAAACTCTC
 GGAAGGGACC AAATGGAAAA AAGACCTTTT TCGGGTTGAC CTGAGGTCAG TCATCCTTTC ACGGTGTTAA CAGTGTACTG GCCATGACCT TCTTTGAGAG
 1501 CCATCCAACA TCACCCAGTG GATGGAACAT CCTGTAACTT TTCACTGCAC TTGGCATTAT TTTTATAAGC TGAATGTGAT AATAAGGACA CTATGGAAT
 GGTAGGTTGT AGTGGGTCAC CTACCTTGTA GGACATTGAA AAGTGACGTG AACCCTAATA AAAATATTTCG ACTTACACTA TTATTCTCTGT GATACCTTTA
 1601 GTCTGGATCA TTCCGTTTTGT GCGTACTTTG AGATTGGTT TGGGATGTC TGTTTTTCAC AGCACTTTTT TATCCTAATG TAAATGCTTT ATTTATTTAT
 CAGACCTAGT AAGGCAACA CGCATGAAAC TCTAAACCAA ACCCTACAGT AACAAAAGTG TCGTGAAAAA ATAGGATTAC ATTACGAAA TAAATAAATA
 1701 TTGGGTACA TTGTAAGATC CATCTACAAA AAAAAAAG GCGGCGCGG ACTCTAGAGT CGACCTGCAG AAGCTTGGCC GCCATGGCC
 AACCCGATGT AACATTCTAG GTAGATGTTT TTTTTTTTTT TTTTTTTTTT CCGCCGCGG TGAGATCTCA CTTGGACGTC TTCGAAACCGG CGGTACCGG

FIG. 1B

1 MEORGONAPAAAGARKRHGPGPREARGARGLRVPKTLVLVAAVLLLVSAESALITQQD
61 LAPQORAAPOQKRSSPSEGLCPPGHHISEDGRDCISCKYQDYSTHWNDLLFCLRCRTRCD
121 SGEVELSPCTTTRNTVCQCEEGTFREEDSPENCRKCRGTGCPRGWVKVGDCTPWSDIECVH
181 KESGIIIGVTVAAVLIVAVFVCKSLMVKVLPYLKGCISGGGGDPERVDRSSQRPGEAD
241 NVLNEIVSILQPTQVPEQEMEVEQPEAPTGVNMLSPGESEHLLLEPAEAERSQRRRLVPA
301 NEGDPTETLRQCFFDDFADLVPFDSWEPLMRKLGMDNEIKVAKAEAGHRDTLYTMLIKW
361 VNKTGRDASVHTLLDALETLGERLAKQKIEDHLLSSGKFMYLEGNADSALS

FIG._2A

Apo2	FADLV	VPFDS	WEP	LMR	KKLG	LM	DNE	IK	VAK	EA	AA	-	GHR	DTL
DR4	FANIV	PFDS	WDL	MRQ	LDL	TKNE	ID	VV	RAG	TA	-	-	GP	DAL
Apo3/DR3	VMDA	VPA	RRW	KKE	FVR	TGL	RE	EA	EA	VE	IG	-	FR	DQQ
TNFR1	VVEN	VPP	PLR	WKE	FVR	RLG	LS	DH	EL	EL	QNG	-	CL	REA
Fas/Apo1	IAGV	MTLS	QVK	G	FVR	KN	G	VNE	AK	IDE	IK	ND	NV	QDTAEQKV

Apo2	YTM	LI	KW	VN	KT	GR	D	-	AS	VH	TL	LD	AL	ET	LG	ER	LAK	QK	IED
DR4	YAM	LM	KW	VN	KT	GR	N	-	AS	IH	TL	LD	AL	ER	ME	ER	HA	KE	KIQD
Apo3/DR3	YEM	LK	RW	RQ	QP	-	-	-	AG	LG	AV	YA	AL	ER	MG	LD	GC	VE	DLRS
TNFR1	YSM	LA	TW	RR	RR	TP	RR	EA	T	LE	LG	RV	LR	DM	MD	LL	GC	LE	DEE
Fas/Apo1	-	QL	LR	NW	HQ	LH	GK	KE	AY	-	DT	LI	KD	LL	KK	AN	CT	LA	EKIQT

FIG._2B

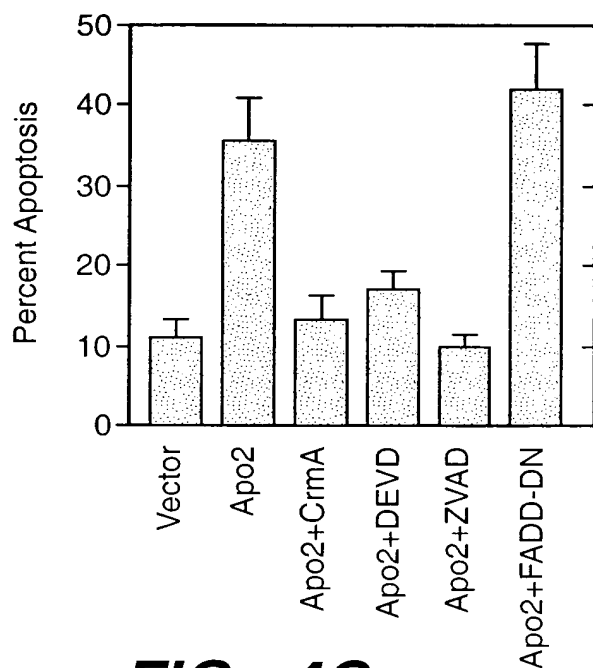


FIG. 4C

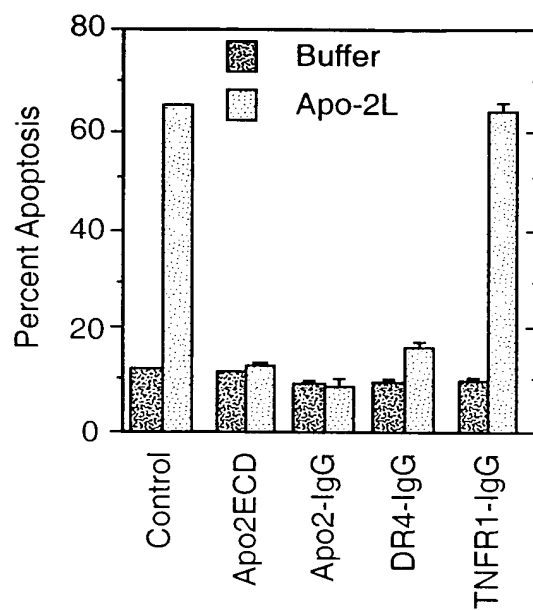


FIG. 4D

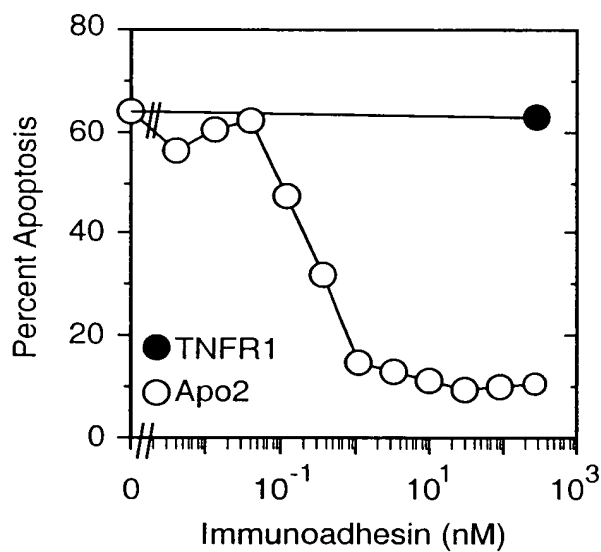


FIG. 4E

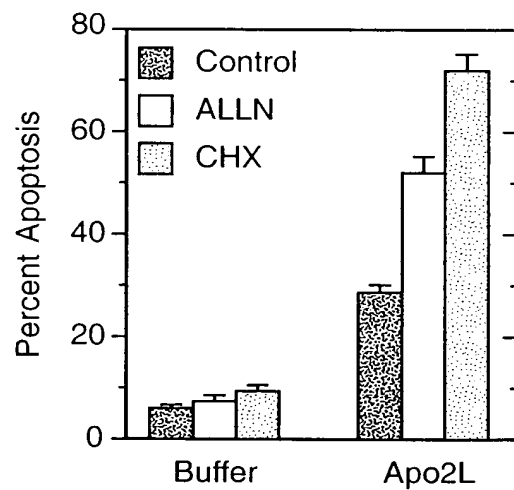


FIG. 5C

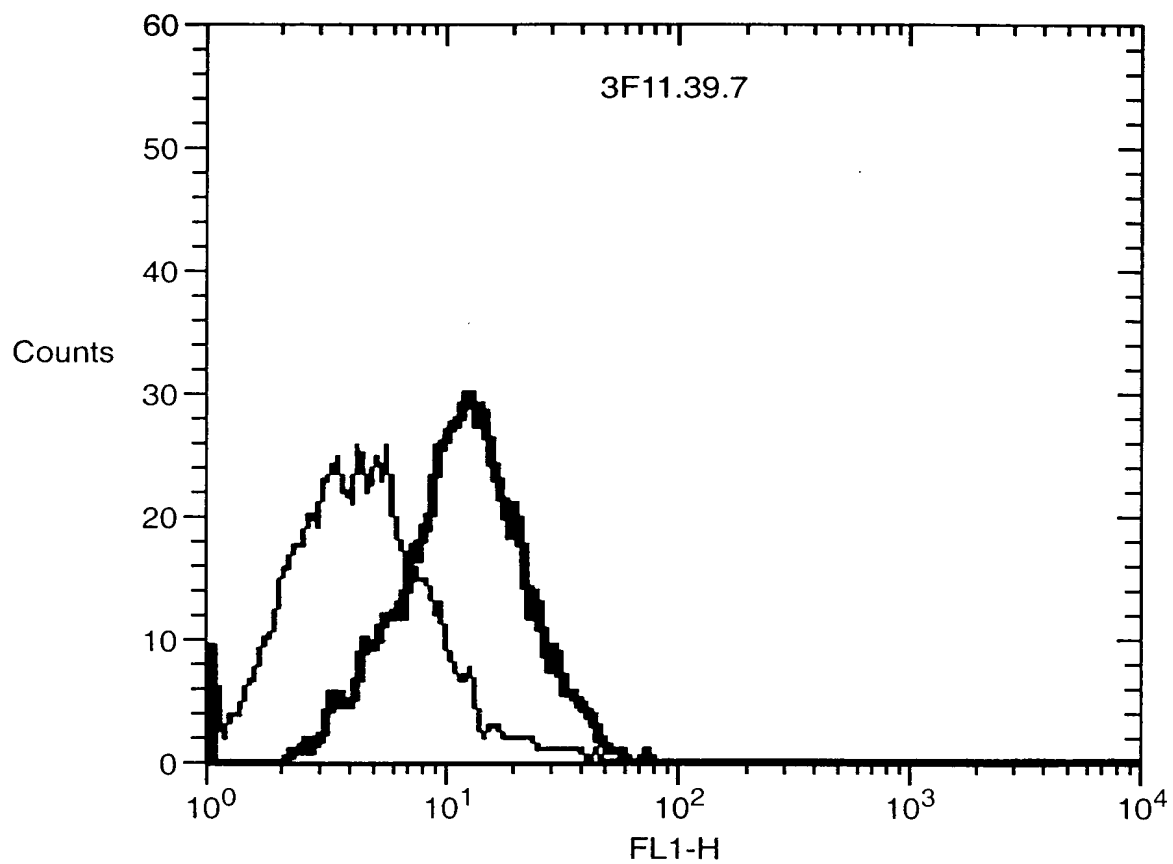


FIG._7

+

FIG._8

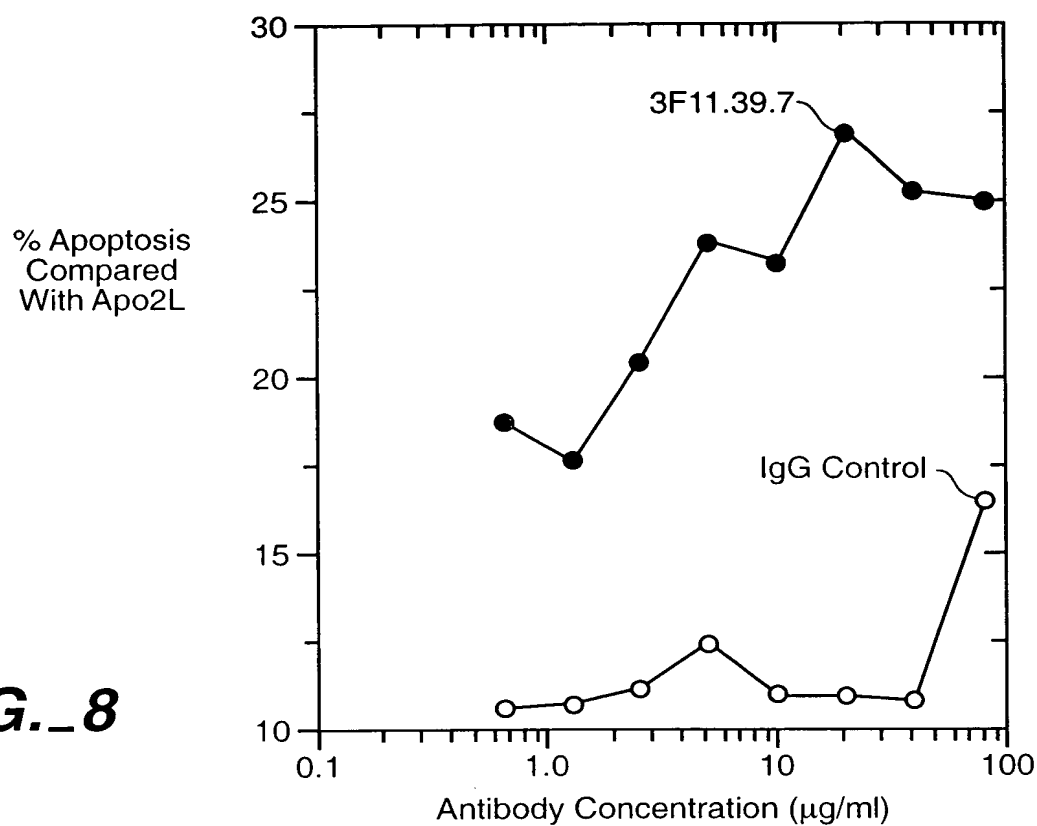


FIG._9

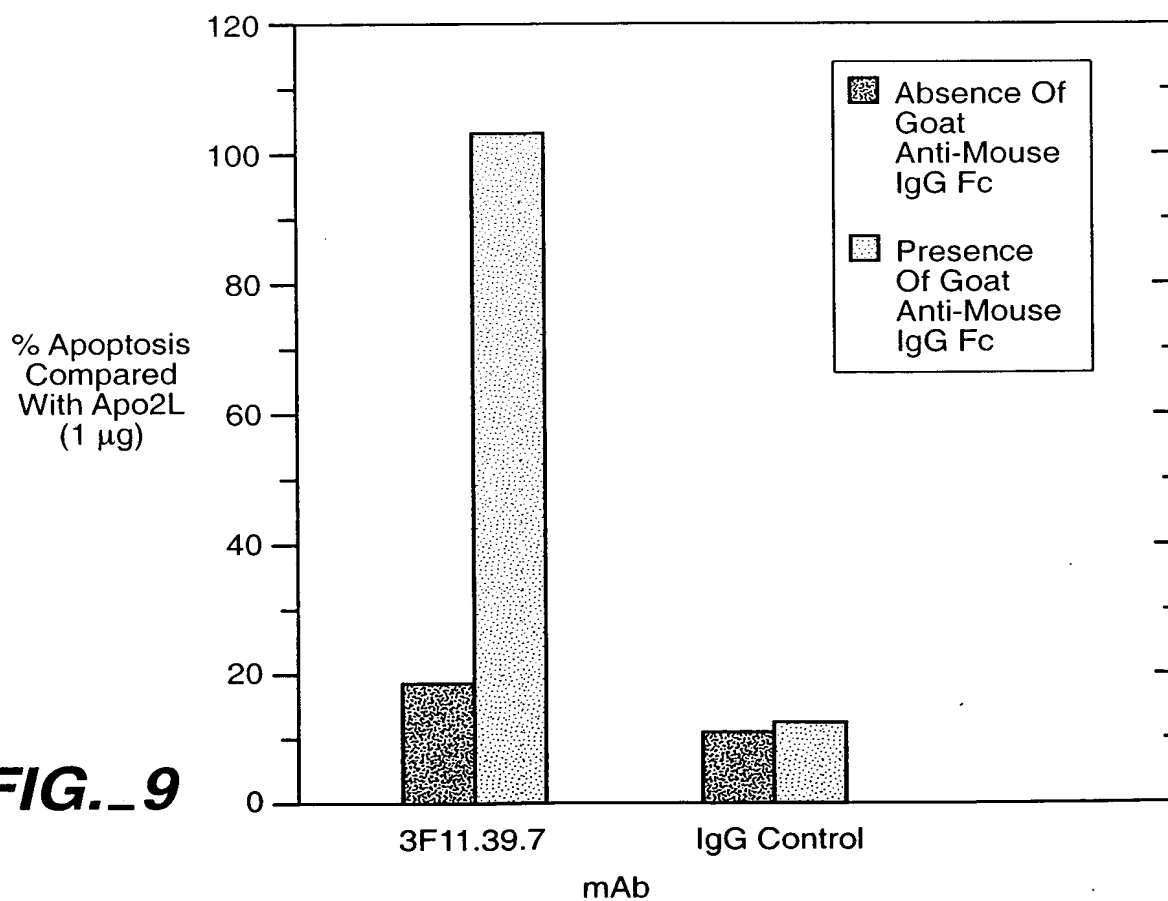


FIG._10

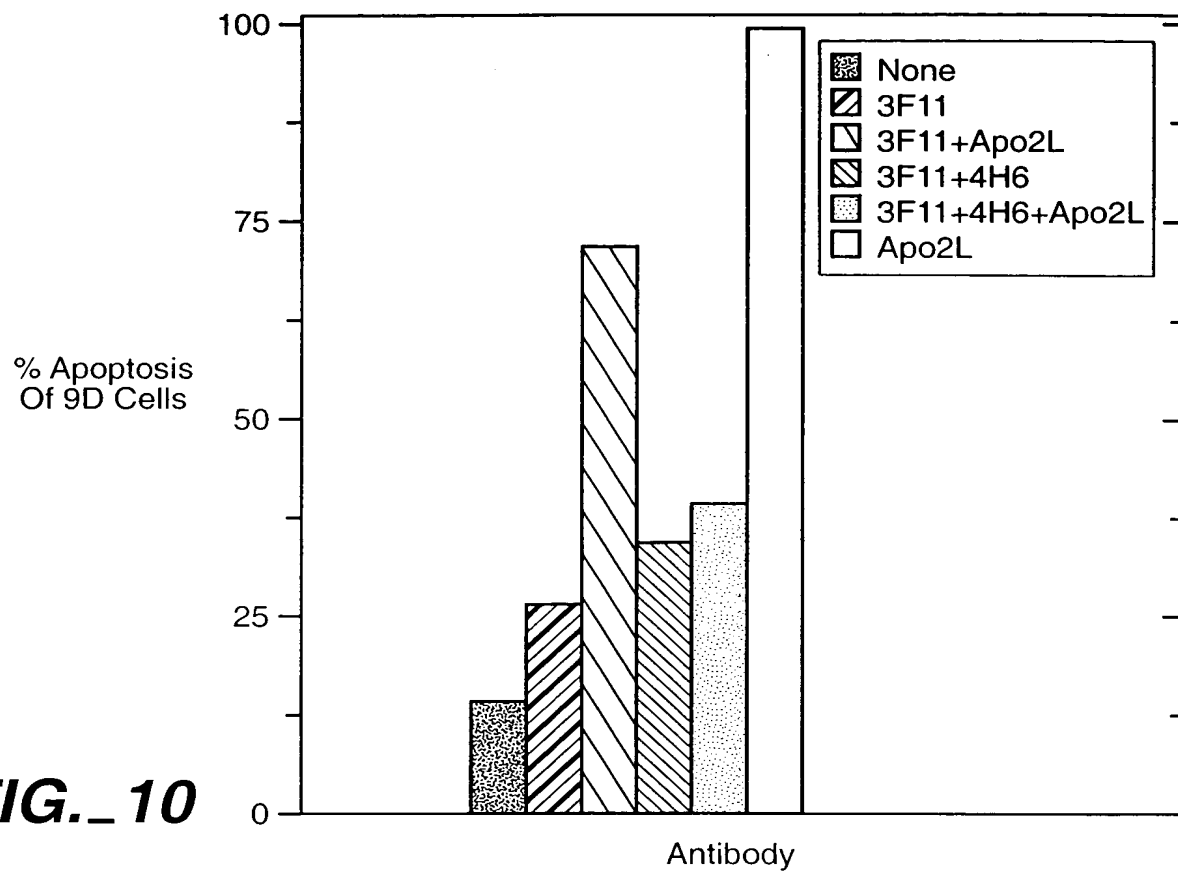
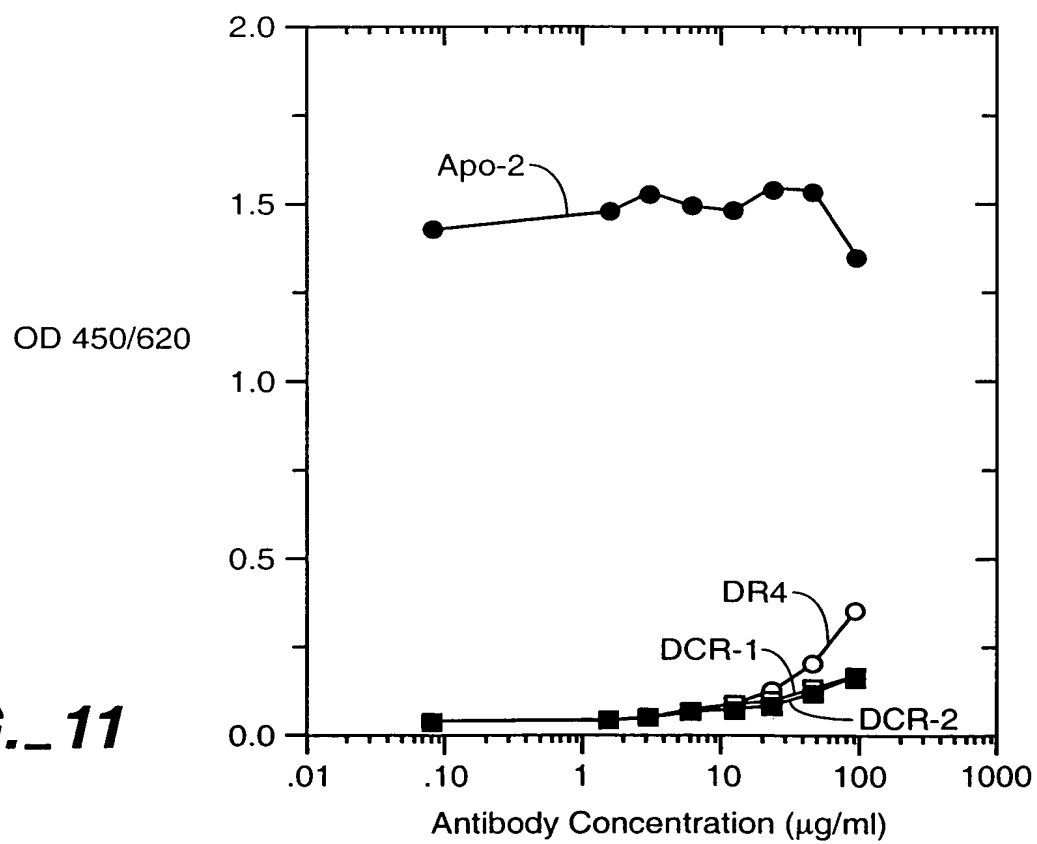
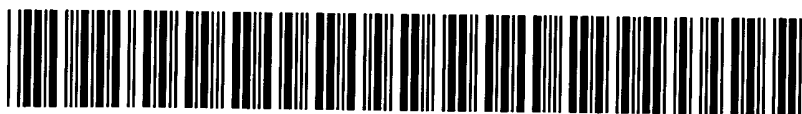


FIG._11





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